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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/539,110	04/19/2006	Gregory I. Frost	DELIA1330-I	9011
28213	7590	03/24/2008	EXAMINER	
DLA PIPER US LLP 4365 EXECUTIVE DRIVE SUITE 1100 SAN DIEGO, CA 92121-2133			CHOWDHURY, IQBAL HOSSAIN	
ART UNIT		PAPER NUMBER		
1652				
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**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

<b>Office Action Summary</b>	<b>Application No.</b>	<b>Applicant(s)</b>	
	10/539,110	FROST ET AL.	
Examiner	Art Unit		
IQBAL H. CHOWDHURY	1652		

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

## Status

1)  Responsive to communication(s) filed on 03 December 2007.

2a)  This action is **FINAL**.                            2b)  This action is non-final.

3)  Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

## **Disposition of Claims**

4)  Claim(s) 1-56 is/are pending in the application.  
4a) Of the above claim(s) 2,3,10,11,16-21,23-49 and 51-56 is/are withdrawn from consideration.  
5)  Claim(s) \_\_\_\_\_ is/are allowed.  
6)  Claim(s) 1, 4-9, 12-15, 22 and 50 is/are rejected.  
7)  Claim(s) \_\_\_\_\_ is/are objected to.  
8)  Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

## Application Papers

9)  The specification is objected to by the Examiner.

10)  The drawing(s) filed on \_\_\_\_\_ is/are: a)  accepted or b)  objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)  The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

12)  Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).  
a)  All b)  Some \* c)  None of:  
1.  Certified copies of the priority documents have been received.  
2.  Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.  
3.  Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

1)  Notice of References Cited (PTO-892)  
2)  Notice of Draftsperson's Patent Drawing Review (PTO-948)  
3)  Information Disclosure Statement(s) (PTO/SB/08)  
Paper No(s)/Mail Date \_\_\_\_\_.  
4)  Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_.  
5)  Notice of Informal Patent Application  
6)  Other: \_\_\_\_\_.  
\_\_\_\_\_

**DETAILED ACTION**

Claims 1-56 are currently pending in the instant application.

This application is a 371 of PCT/US03/40090.

The preliminary amendment filed on June 13, 2005, amending claim 23 is acknowledged.

*Election/Restriction*

Applicant's election with traverse of Group I, Claims 1-22 and 50, drawn to an isolated polypeptide chondroitinase glycoprotein (CHASEGP) and a composition comprising said polypeptide, and protein of SEQ ID NO: 6 and nucleic acid encoding SEQ ID NO: 6, in the communication filed on December 3, 2007 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the Restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)). It is to be mentioned here that SEQ ID NO: 6 is not a species but a specific invention as an independent and distinct protein.

Claims 2-3, 10-11, 16, 23-49 and 51-56 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention. Claims 17-21 are also withdrawn because claims encompass mutants and variants of SEQ ID NO: 6 because each of the mutants and variants are structurally independent and distinct protein. Besides, the mutants and variants do not share any special technical feature with wild type chondroitinase protein, as wild type chondroitinase protein is known in the art (see previous Office action).

Claims 1, 4-9, 12-15, 22, and 50 are under consideration and will be examined herein.

***Priority***

Acknowledgement is made of applicants claim for priority of provisional application 60/433,532 filed on 12/16/2002.

***Information Disclosure Statement***

There is no information disclosure statement (IDS) with this application.

***Drawings***

There is no drawing with this application.

***Claim Objections***

Claims 1, 9, 13-14, 22, and 50 are objected to in the recitation of “CHASEGP” as abbreviations should not be used without at least once fully setting forth what they are used for. Appropriate correction is required.

Claim 4 is objected to in the recitation of “PNGase” as abbreviations should not be used without at least once fully setting forth what they are used for. Appropriate correction is required.

Claim 8 is objected to in the recitation of “sialylic acid”, which is not a common expression that should be “sialic acid”. Appropriate correction is required.

Claims 4-9 and 14 are objected to in the recitation of “claim-1”, which should be “claim 1”. Appropriate correction is required.

Claim 14 is objected to in the recitation of “as described in SEQ ID NO: 6”, which should

be "as set forth in SEQ ID NO: 6". Appropriate correction is required.

Claim 9 is objected to in the recitation "A substantially purified glycoprotein", which should be "The substantially purified glycoprotein". Appropriate correction is required.

Claim 12 is objected to in the recitation "A polypeptide", which should be "The polypeptide". Appropriate correction is required.

### ***Claim Rejections - 35 USC § 101***

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1, 9, and 12-15 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claims 1, 9 and 12-15 recite "A ---- chondroitinase glycoprotein" or "A polypeptide", which reads on a naturally occurring chondroitinase glycoprotein or polypeptide. Naturally occurring polypeptide is not patentable.

In the absence of the hand of man, naturally occurring nucleic acids and /or proteins are considered non-statutory subject matter. *Diamond and Chakrabarty*, 206 USPQ 193 (1980). This rejection may be overcome by amending the claims to contain wording such as "An isolated glycoprotein or polypeptide". For examination purpose the claim is read as such.

### ***Claim Rejections - 35 USC § 112***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter, which the applicant regards as his invention.

Claims 1, 4-9, 12-15, 22 and 50 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite and vague for failing to particularly point out and distinctly claim the subject

matter which applicant regards as the invention. Claims 1, 9, 13, 22 and 50 are indefinite in the recitation of “substantially purified or pure” as it is unclear how purified or pure of a polypeptide must be to be encompassed by the phrase “substantially purified or pure”. While page 31 attempts to define “substantially pure”, however, the description is not a clear definition. Therefore, it is not clear to the Examiner as to how much pure of the protein is encompassed in the above phrase. Accordingly, claims 4-8, 12, 14-15, and 17-21 are rejected, as they depend on claim 1.

***Claim Rejections - 35 USC § 112***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1, 4-9, 13 and 50 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter, which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1, 4-9, 13, 22 and 50 are directed to a soluble chondroitinase glycoprotein and a composition comprising said chondroitinase glycoprotein.

The Court of Appeals for the Federal Circuit has recently held that a “written description of an invention involving a chemical genus, like a description of a chemical species, ‘requires a precise definition, such as by structure, formula [or] chemical name,’ of the claimed subject matter sufficient to distinguish it from other materials.” University of California v. Eli Lilly and

Co., 1997 U.S. App. LEXIS 18221, at \*23, quoting *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993). To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these (paraphrased from *Enzo Biochemical*).

Thus, claims 1, 4-9, 13, 22 and 50 are directed to any chondroitinase glycoprotein having any structure isolated from any source and a composition comprising said chondroitinase glycoprotein polypeptide.

Claims are thus drawn to any chondroitinase glycoprotein isolated from any source and a composition comprising said chondroitinase glycoprotein, wherein said proteins structures are not fully described in the specification. No information, beyond the characterization of a protein having activity of degrading chondroitin, which would indicate that applicants had possession of the claimed genus of any chondroitinase glycoprotein and a composition comprising said chondroitinase. The specification does not also contain any disclosure of the structure of all the mutants or variants of any chondroitinase glycoprotein and a composition comprising said chondroitinase glycoprotein in the claims. The genus of proteins (any chondroitinase glycoprotein) as claimed is a large variable genus including many mutants and variants, which can have wide variety of structures. Therefore, many structurally unrelated proteins are encompassed within the scope of the claims. The specification discloses the structure of only

three representative species of the claimed genus (SEQ ID NO: 1, 2 and 6), which is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus. Therefore, one skilled in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time the instant application was filed.

Applicant is referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at [www.uspto.gov](http://www.uspto.gov).

Claims 1, 4-9, 12-13, 15, 22 and 50 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a chondroitinase glycoprotein of SEQ ID NO: 6 having chondroitinase domain and a composition comprising said chondroitinase glycoprotein of SEQ ID NO: 6, wherein the encoded nucleic acids can hybridizes under high stringency condition to full length of SEQ ID NO: 3 or 5, does not reasonably provide enablement for any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least any one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the claimed invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation is required are summarized in *In re Wands* (858 F.2d 731,737, 8 USPQ2nd 1400 (Fed. Cir. 1988)) as follows:

(1) quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence and absence of working examples, (4) the nature of the invention, (5) the state of prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. The factors, which have, lead the Examiner to conclude that the specification fails to teach how to make and/or use the claimed invention without undue experimentation, are addressed below:

**The breadth of the claims:**

Claims 1, 4-9, 12-13, 15, 22 and 50 are so broad as to encompass any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure.

The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the extremely large number of proteins having chondroitin degrading activity, which includes many mutants and variants broadly encompassed by the claims. However, in this case the disclosure is limited to the nucleotide and encoded amino acid sequence of only three chondroitinase glycoproteins i.e. SEQ ID NO: 1, 2 and 6.

**The quantity of experimentation required practicing the claimed invention based on the teachings of the specification:**

While methods of generating or isolating variants of a polypeptide were well known in

the art at the time of invention, it is not routine in the art to screen by trial and error process for (1) any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure, (2) an essentially infinite number of mutations of any chondroitinase glycoprotein amino acid sequence. The amino acids modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple point mutations or substitutions. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification.

**The state of prior art, the relative skill of those in the art, and the predictability or unpredictability of the art:**

The amino acid sequence of a polypeptide determines its structural and functional properties. While the specification discloses three chondroitinase glycoprotein, neither the specification nor the art provide a correlation between structure and function such that one of skill in the art can envision the structure of any chondroitinase glycoprotein or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high

stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least any one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein as claimed. The art clearly teaches that modification of a protein's amino acid sequence to obtain the desired activity without any guidance/knowledge as to which amino acids in a protein are tolerant of modification and which ones are conserved is highly unpredictable. At the time of the invention there was a high level of unpredictability associated with altering a polypeptide sequence with an expectation that the polypeptide will maintain the desired activity. For example, Branden et al. (1991) teach that (1) protein engineers are frequently surprised by the range of effects caused by single mutations that they hoped would change only one specific and simple property in enzymes, (2) the often surprising results obtained by experiments where single mutations are made reveal how little is known about the rules of protein stability, and (3) the difficulties in designing de novo stable proteins with specific functions. The teachings of Branden et al. are further supported by the teachings of Witkowski et al. (1999) and Seffernick et al. (2001), where it is shown that even small amino acid changes result in enzymatic activity changes.

**The amount of direction or guidance presented and the existence of working examples:**

The specification discloses a chondroitinase glycoprotein of SEQ ID NO: 6 having chondroitinase domain and a composition comprising said chondroitinase glycoprotein of SEQ ID NO: 6, wherein the encoded nucleic acids can hybridizes under high stringency condition to full length sequence of SEQ ID NO: 3 or 5. However, the specification fails to provide any clue as to the structural elements required in any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any

polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure or which are the structural elements in said proteins known in the art that are essential for successfully practice the claimed invention. No correlation between structure and function has been presented.

The specification does not support the broad scope of the claims which encompass any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure because the specification does not establish: (A) regions of the protein structure which may be modified without affecting chondroitinase activity and; (B) the general tolerance of chondroitinase glycoprotein to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any chondroitinase glycoprotein amino acid residues with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and/or use the claimed invention in a manner reasonably correlated with the scope of

the claims broadly including any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure. The scope of the claims must bear a reasonable correlation with the scope of enablement (In re Fisher, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of a chondroitinase glycoprotein or a chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising said chondroitinase glycoprotein having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

### ***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an

international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1, 4-9, 12-15, 22 and 50 are rejected under 35 U.S.C. 102(e) as being anticipated by Bodary et al. (WO 2004/028479-A2, publication 4/8/2004, claim priority of US application 60/414,006 filed on 9/25/2002). Instant claims drawn to any chondroitinase glycoprotein having any structure or any chondroitinase glycoprotein having any catalytically active portion thereof or any polypeptide having chondroitinase domain, wherein the encoded nucleic acids hybridizes under high stringency conditions at least 70% of its full length of nucleotides 726-1995 in SEQ ID NO: 3 or SEQ ID NO: 5 or at least one domain thereof or any catalytically active portion of the domain and a composition comprising any chondroitinase glycoprotein having any structure.

Bodary et al. disclose a protein, which is 100% identical to the SEQ ID NO: 6 of the instant application (see sequence alignment), inherently a chondroitinase glycoprotein. Bodary et al. also teach a composition comprising said protein. Since, the protein of Bodary et al. is 100% identical to SEQ IDNO: 6 of the instant application, said protein would inherently comprise the chondroitinase domain and catalytic domain. Bodary et al. further disclose nucleic acid sequence encoding said protein which is 100% identical to SEQ ID NO: 3 and 5 of the instant application (see sequence alignment). The nucleic acid sequence of the Bodary et al., which is 100% identical to SEQ ID NO: 3 and 5, would hybridize with the recited sequences of SEQ ID NO: 3 and 5 or any fragments thereof of the instant application. Bodary et al. furthermore, disclose cloning the gene encoding protein in an expression vector and express in *E. coli* and CHO mammalian cells, followed by purification. Because, the protein is expressed in mammalian CHO cells, the protein would be glycosylated, wherein asparagine residue is the common

glycosylation site, wherein said glycosidic bond would be inherently sensitive to PNGase, since, PNGase hydrolyze glycosidic bond. In mammalian cells, when the protein is glycosylated, the glycosyl residues usually comprise complex sugar molecules.

Because the glycosylated protein of the instant application (claims 7 and 8) and the glycosylated protein (which is expressed in the mammalian CHO cells) of the reference is one and the same, Examiner takes the position that the glycosylated protein disclosed in the reference inherently has hybrid type of sugar molecule would terminated with sialic acid molecule as claimed in claim 7-8. Since the Office does not have the facilities for examining and comparing applicants' glycosylated protein with the glycosylated protein disclosed by the prior art, the burden is on the applicant to show a novel or unobvious difference between the claimed product (i.e. glycosylated) and the product of the prior art (i.e., glycosylated). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594. Therefore, Bodary et al. anticipate claims 1, 4-9, 12-15, 22 and 50 of the instant application.

### ***Conclusion***

#### **Status of the claims:**

Claims 1-56 are pending.

Claims 2-3, 10-11, 16-21, 23-49, 51-56 are withdrawn.

Claims 1, 4-9, 12-15, 22 and 50 are rejected.

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Iqbal Chowdhury whose telephone number is 571-272-8137. The examiner can normally be reached on 9:00-5:00 PM.

Art Unit: 1652

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy can be reached on 703-272-0928. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



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<!--StartFragment-->RESULT 1

ADN05873

ID ADN05873 standard; cDNA; 2414 BP.

XX

AC ADN05873;

XX

DT 11-JUN-2007 (revised)

DT 01-JUL-2004 (first entry)

XX

DE Antipsoriatic cDNA sequence #1168.

XX

KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.

XX

OS Homo sapiens.

XX

PN WO2004028479-A2.

XX

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-US030907.

XX

PR 25-SEP-2002; 2002US-0414006P.

XX

PA (GETH ) GENENTECH INC.

XX

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu TD;

XX

DR WPI; 2004-305105/28.

DR P-PSDB; ADN05874.

DR PC:NCBI; gi6912427.

DR PC\_ENCPRO:NCBI; gi6912428.

XX

PT New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a mammal.

XX

PS Claim 1; SEQ ID NO 2268; 3069pp; English.

XX

CC The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 2414 BP; 672 A; 475 C; 504 G; 763 T; 0 U; 0 Other;

Query Match 100.0%; Score 1446; DB 12; Length 2414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAGTATTATCTGAAGGACAGTAAAGCTTGTGTTCAACCAGTACATCTCACT 60  
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 642 ATGAAAGTATTATCTGAAGGACAGTAAAGCTTGTGTTCAACCAGTACATCTCACT 701

Qy 61 TCATGGCTCCTTATATTTTATTCTAAAGTCTATCTCTTGTCTAAAACCTGCTCGACTT 120  
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 702 TCATGGCTCCTTATATTTTATTCTAAAGTCTATCTCTTGTCTAAAACCTGCTCGACTT 761

Qy	121	CCAATTATCAAAGGAAACCTTTATAGCTGCTTGAATGCTCCAACAGATCAGTGTG 180
Db	762	
Qy	181	ATAAAATATAATTAAAGACTAAATTGAAAATGTTCTGTGATTGGAAGCCCCTGGCC 240
Db	822	
Qy	241	AAGGCCAGGGGGCAAAATGTCACTATATTATGTCAACAGATTGGGATACTATCCGTGG 300
Db	882	
Qy	301	TATACATCACAGGGGTCCCCATTAATGGAGGTCTCCCACAGAACATAAGTTACAAGTA 360
Db	942	
Qy	361	CATCTGGAAAAAGCTGACCAAGATATTAATTACATCCCTGCTGAAGATTTCAGTGG 420
Db	1002	
Qy	421	CTTGCTGTTATAGATTGGAATATTGGAGACCACAGTGGCCCGGAACTGGAACCTCAAA 480
Db	1062	
Qy	481	GATGTTACAGACAGAAGTCAGAACAGCTTATTCGATATGGAAAGAACATGATCAGCT 540
Db	1122	
Qy	541	ACCGATATTGAATATTAGCCAAAGTGACCTTGAGAAAGTGCAGAACAGCTTCATGAAG 600
Db	1182	
Qy	601	GAAACCATCAAATTGGAATTAAGAGCCGACCCAAAGGCCCTTGGGTTATTATTATAT 660
Db	1242	
Qy	661	CCTGATTGCCACAATTATAACGTTATGCCCAAACACTCTGGGTATGCCAGAAC 720
Db	1302	
Qy	721	GAAGTCTTGAGGAACAATGAGCTCTTGGCTCTGGAACAGCAGTGCTGCTTATATCCT 780
Db	1362	
Qy	781	1421 GAAGTCTTGAGGAACAATGAGCTCTTGGCTCTGGAACAGCAGTGCTGCTTATATCCT 1421
Db	1422	
Qy	841	TCTATCTGTCTGGAAATCCCTTGAGACAGTGAAACATTTGCCTCTCAAATT 840
Db	1482	
Qy	901	TCTATCTGTCTGGAAATCCCTTGAGACAGTGAAACCTTATTTGCCTCTCAAATT 960
Db	1542	
Qy	961	1601 TCTATCTGTCTGGAAATCCCTTGAGACAGTGAAACCTTATTTGCCTCTCAAAGAT 1601
Db	1602	

Qy	1021	GACATGAATTAACTGCATCCAAGGCCAACTGTACAAAGGTGAAGCAGTTGTGAGTTCT	1080
Db	1662	GACATGAATTAACTGCATCCAAGGCCAACTGTACAAAGGTGAAGCAGTTGTGAGTTCT	1721
Qy	1081	GATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTGAGGTATGCAGCCTCACCTC	1140
Db	1722	GATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTGAGGTATGCAGCCTCACCTC	1781
Qy	1141	TGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACGCCAGTTACCTCACTTG	1200
Db	1782	TGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACGCCAGTTACCTCACTTG	1841
Qy	1201	AACCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGAGTTACTGTGAAAGGAAAA	1260
Db	1842	AACCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGAGTTACTGTGAAAGGAAAA	1901
Qy	1261	GCATCTGATAACAGACCTGGCAGTGATGGCAGATACTTTCTGTCAATTGTTATCAGGGA	1320
Db	1902	GCATCTGATAACAGACCTGGCAGTGATGGCAGATACTTTCTGTCAATTGTTATCAGGGA	1961
Qy	1321	TATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATGGCTGCTGGGTTCCCT	1380
Db	1962	TATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATGGCTGCTGGGTTCCCT	2021
Qy	1381	TCTCCTGGTCACTAATGACACTTGTCTACTGCTTTAGCAAGTTATCGAACGATTCAAG	1440
Db	2022	TCTCCTGGTCACTAATGACACTTGTCTACTGCTTTAGCAAGTTATCGAACGATTCAAG	2081
Qy	1441	TTGTGA 1446	
Db	2082	TTGTGA 2087	

<!--EndFragment-->

#5

<!--StartFragment-->RESULT 2

ADN05873

ID ADN05873 standard; cDNA; 2414 BP.

XX

AC ADN05873;

XX

DT 11-JUN-2007 (revised)

DT 01-JUL-2004 (first entry)

XX

DE Antipsoriatic cDNA sequence #1168.

XX

KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.

XX

OS Homo sapiens.

XX

PN WO2004028479-A2.

XX

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-US030907.

XX

PR 25-SEP-2002; 2002US-0414006P.

XX

PA (GETH ) GENENTECH INC.

XX

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu TD;

XX

DR WPI; 2004-305105/28.

DR P-PSDB; ADN05874.

DR PC:NCBI; gi6912427.

DR PC\_ENCPRO:NCBI; gi6912428.

XX

PT New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a mammal.

XX

PS Claim 1; SEQ ID NO 2268; 3069pp; English.

XX

CC The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 2414 BP; 672 A; 475 C; 504 G; 763 T; 0 U; 0 Other;

Query Match 100.0%; Score 1269; DB 12; Length 2414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAAACCTGCTCGACTTCCAATTATCAAAGGAAACCTTTATAGCTGCTTGGAAATGCT 60  
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 744 CTAAAACCTGCTCGACTTCCAATTATCAAAGGAAACCTTTATAGCTGCTTGGAAATGCT 803

Qy 61 CCAACAGATCAGTGGATAAAATATAATTAAAGACTAAATTGAAAATGTTCTGTG 120  
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 804 CCAACAGATCAGTGGATAAAATATAATTAAAGACTAAATTGAAAATGTTCTGTG 863

Qy	121	ATTGGAAAGCCC ACTGGCCAAGGCCAGGGGGCAAAATGTC ACTATATTTATGTC AACAGA	180
Db	864	ATTGGAAAGCCC ACTGGCCAAGGCCAGGGGGCAAAATGTC ACTATATTTATGTC AACAGA	923
Qy	181	TTGGGATACTATCCGTGGTACATCACAGGGGTCCCCATTAAATGGAGGTCTCCACAG	240
Db	924	TTGGGATACTATCCGTGGTACATCACAGGGGTCCCCATTAAATGGAGGTCTCCACAG	983
Qy	241	AACATAAGTTACAAGTACATCTGGAAAAGCTGACCAAGATATTAATTACATCCCT	300
Db	984	AACATAAGTTACAAGTACATCTGGAAAAGCTGACCAAGATATTAATTACATCCCT	1043
Qy	301	GCTGAAGATTCAGTGGACTTGCTGTATAGATTGGAATTGGAGACCACAGTGGCC	360
Db	1044	GCTGAAGATTCAGTGGACTTGCTGTATAGATTGGAATTGGAGACCACAGTGGCC	1103
Qy	361	CGGAACTGGAACTCAAAAGATGTTACAGACAGAAGTCAAGAAAGCTTATTCCGATATG	420
Db	1104	CGGAACTGGAACTCAAAAGATGTTACAGACAGAAGTCAAGAAAGCTTATTCCGATATG	1163
Qy	421	GGAAAGAATGTATCAGCTACCGATATTGAATATTAGCCAAGTGACCTTGAAGAAAGT	480
Db	1164	GGAAAGAATGTATCAGCTACCGATATTGAATATTAGCCAAGTGACCTTGAAGAAAGT	1223
Qy	481	GCAAAAGCTTCATGAAGGAAACCATCAAATTGGAATTAAAGAGCCGACCCAAAGGCCTT	540
Db	1224	GCAAAAGCTTCATGAAGGAAACCATCAAATTGGAATTAAAGAGCCGACCCAAAGGCCTT	1283
Qy	541	TGGGGTTATTATTTATCCTGATTGCCACAATTATAACGTTATGCCCAAACACTACTCT	600
Db	1284	TGGGGTTATTATTTATCCTGATTGCCACAATTATAACGTTATGCCCAAACACTACTCT	1343
Qy	601	GGGTCATGCCAGAAGACGAACTTGGAGAACAAATGAGCTCTGGCTCTGGAACAGC	660
Db	1344	GGGTCATGCCAGAAGACGAAGTCTTGGAGAACAAATGAGCTCTGGCTCTGGAACAGC	1403
Qy	661	AGTGCTGCTTATATCCTCTATCTGTGTCTGGAAATCCCTGGAGACAGTGAAACATT	720
Db	1404	AGTGCTGCTTATATCCTCTATCTGTGTCTGGAAATCCCTGGAGACAGTGAAACATT	1463
Qy	721	TTGCGCTTCTCCAAATTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTCAT	780
Db	1464	TTGCGCTTCTCCAAATTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTCAT	1523
Qy	781	GATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTATTT	840
Db	1524	GATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTATTT	1583
Qy	841	TTCCCTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCCTGGAGCTGCA	900
Db	1584	TTCCCTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCCTGGAGCTGCA	1643
Qy	901	GGCATTGTTATTGGGGAGACATGAATTAACTGCATCCAAGGCCAACTGTACAAAGGTG	960
Db	1644	GGCATTGTTATTGGGGAGACATGAATTAACTGCATCCAAGGCCAACTGTACAAAGGTG	1703
Qy	961	AAGCAGTTGTGAGTTCTGATTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTGAG	1020
Db	1704	AAGCAGTTGTGAGTTCTGATTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTGAG	1763

Qy	1021	GTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACGCG	1080
Db	1764	GTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACGCG	1823
Qy	1081	CCCAGTTACCTTCACTTGAACCCCTGCAAGTTACACATAGAGGCCTCTGAGGACGGGAG	1140
Db	1824	CCCAGTTACCTTCACTTGAACCCCTGCAAGTTACACATAGAGGCCTCTGAGGACGGGAG	1883
Qy	1141	TTTACTGTGAAAGGAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACTTTCC	1200
Db	1884	TTTACTGTGAAAGGAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACTTTCC	1943
Qy	1201	TGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATGGC	1260
Db	1944	TGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATGGC	2003
Qy	1261	TGCTCTGGG	1269
Db	2004	TGCTCTGGG	2012

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<!--StartFragment-->RESULT 2  
 ADN05874  
 ID ADN05874 standard; protein; 481 AA.  
 XX  
 AC ADN05874;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Antipsoriatic protein sequence #1100.  
 XX  
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004028479-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030907.  
 XX  
 PR 25-SEP-2002; 2002US-0414006P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 DR WPI; 2004-305105/28.  
 DR N-PSDB; ADN05873.  
 XX  
 PT New PRO nucleic acid or polypeptide, useful for preparing a  
 PT pharmaceutical composition for diagnosing or treating psoriasis in a  
 PT mammal.  
 XX  
 PS Claim 9; SEQ ID NO 2269; 3069pp; English.  
 XX  
 CC The invention relates to novel polynucleotide and polypeptides for  
 CC treating psoriasis or a sequence having at least 80% identity to the  
 CC above sequences. The nucleic acid is useful for preparing a composition  
 CC for diagnosing or treating psoriasis in a mammal. This sequence  
 CC corresponds to one of the polypeptides of the invention.  
 XX  
 SQ Sequence 481 AA;

Query Match 100.0%; Score 2284; DB 8; Length 481;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-207;  
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LKPARLPIYQRKPFIAAWNAPTDQCLIKYNLRLNLKMFPVIGSPLAKARGQNVTFYVNR 60  
 Db 35 LKPARLPIYQRKPFIAAWNAPTDQCLIKYNLRLNLKMFPVIGSPLAKARGQNVTFYVNR 94  
 Qy 61 LGYYPWYTSQGVPINGGLPQNISLQVHLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWA 120  
 Db 95 LGYYPWYTSQGVPINGGLPQNISLQVHLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWA 154  
 Qy 121 RNWNSKDVYRQKSRKLISDMGKNVSATDIEYLAKVTFEESAKAFMKETIKLGIKSRSRKG 180  
 Db 155 RNWNSKDVYRQKSRKLISDMGKNVSATDIEYLAKVTFEESAKAFMKETIKLGIKSRSRKG 214  
 Qy 181 WGYLYPDCHNYNVYAPNYSGSCPDEVLRNNELSWLNSSAALYPSICVWKSLGDSENI 240

Db 215 WGYLYPDCHNYNVYAPNYSGSCPEDEVLRNNELSWLNSSAALYPSICVWKSLGDSENI 274  
Qy 241 LRFSKFRVHESMRISTMTSHDYALPVFVYTRLGYRDEPLFFLSKQDLVSTIGESAALGAA 300  
Db 275 LRFSKFRVHESMRISTMTSHDYALPVFVYTRLGYRDEPLFFLSKQDLVSTIGESAALGAA 334  
Qy 301 GIVIWGDMNLTASKANCTVKQFVSSDLGSYIANVTRAEVCSLHLCRNNGRCIRKMWNA 360  
Db 335 GIVIWGDMNLTASKANCTVKQFVSSDLGSYIANVTRAEVCSLHLCRNNGRCIRKMWNA 394  
Qy 361 PSYLHLNPASYHIEASEDGEFTVKGKASDTDLAVMADTFSCHCYQGYEGADCRIKTAGD 420  
Db 395 PSYLHLNPASYHIEASEDGEFTVKGKASDTDLAVMADTFSCHCYQGYEGADCRIKTAGD 454  
Qy 421 CSG 423  
Db 455 CSG 457  
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